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<u>L3</u>	L1 and (antisense or ribozyme\$) and phosphatase\$	34	<u>L3</u>
<u>L2</u>	L1 same (antisense or ribozyme\$)	0	<u>L2</u>
<u>L1</u>	hvh3 or b23 or dusp5	1522	<u>L1</u>

END OF SEARCH HISTORY

Set Items Description  
S1 0 (DUSP (W) 5)  
S2 23 HVH (W) 3  
S3 5 RD (unique items)  
>>>KWIC option is not available in file(s): 41, 77, 399

3/3,K/1 (Item 1 from file: 5)  
DIALOG(R)File 5:Biosis Previews(R)  
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11605962 BIOSIS NO.: 199800387697

**Changes of gene expression by lysophosphatidylcholine in vascular endothelial cells: 12 Up-regulated distinct genes including 5 cell growth-related, 3 thrombosis-related, and 4 others.**

AUTHOR: Sato Naoaki; Kokame Koichi; Shimokado Kentaro; Kato Hisao; Miyata Toshiyuki(a)

AUTHOR ADDRESS: (a)Natl. Cardiovasc. Cent. Res. Inst., 5-7-1 Fujishirodai, Suita, Osaka 565-8565\*\*Japan

JOURNAL: Journal of Biochemistry (Tokyo) 123 (6):p1119-1126 June, 1998

ISSN: 0021-924X

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

Q P 501.56

...ABSTRACT: and untreated human umbilical vein endothelial cells. We identified 12 up-regulated distinct genes including 5 cell growth-related genes (two phosphatases CL100 and B23/\*hVH\*-\*3\*, gravin, activating transcription factor-4, and heparin-binding epidermal growth factor-like growth factor), 3 thrombosis-related genes (plasminogen activator inhibitor-1, tissue plasminogen activator...

3/3,K/2 (Item 2 from file: 5)  
DIALOG(R)File 5:Biosis Previews(R)  
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10026345 BIOSIS NO.: 199598481263

**The role of dual specificity phosphatase \*HVH\*-\*3\* on ERK regulation during neuronal differentiation.**

AUTHOR: Kwak S P; Dixon J E

AUTHOR ADDRESS: Dep. Biol. Chem., Univ. Michigan, Ann Arbor, MI 48109\*\*USA

JOURNAL: Society for Neuroscience Abstracts 21 (1-3):p808 1995

CONFERENCE/MEETING: 25th Annual Meeting of the Society for Neuroscience San Diego, California, USA November 11-16, 1995

ISSN: 0190-5295

RECORD TYPE: Citation

LANGUAGE: English

**The role of dual specificity phosphatase \*HVH\*-\*3\* on ERK regulation during neuronal differentiation.**

3/3,K/3 (Item 3 from file: 5)  
DIALOG(R)File 5:Biosis Previews(R)  
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09665875 BIOSIS NO.: 199598120793

**Multiple dual specificity protein tyrosine phosphatases are expressed and regulated differently in liver cell lines.**

AUTHOR: Kwak Seung P; Dixon Jack E(a)

AUTHOR ADDRESS: (a)Dep. Biol. Chem., Room 5416, Med. Sci. Building 1, University Michigan, Ann Arbor, MI 48109-0606\*\*USA

JOURNAL: Journal of Biological Chemistry 270 (3):p1156-1160 1995

ISSN: 0021-9258

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

Q P 501.57  
~  
M. Gelin

↓ 269 : 29,897 - 29,902

...ABSTRACT: other PTPases they exhibit dual catalytic activity toward phosphotyrosine and nearby phosphothreonine residues in substrate proteins. We have isolated a novel VH-1-like PTPase, \*hVH\*--\*3\*, from the human placenta and compared various aspects of its expression with previously isolated members of this subfamily. The mammalian members of this subfamily including \*hVH\*--\*3\* commonly localize to the nucleus and exhibit catalytic activity toward phosphorylated extracellular signal-regulated kinase. However, while the expression of some VH-1-like PTPases is extremely transient and independent of protein synthesis, \*hVH\*--\*3\* expression is sustained over 3 h after being cell stimulated. Tissue-specific expression of \*hVH\*--\*3\* is also distinct from other VH-1-like PTPases. Although VH-1-like PTPases have overlapping substrate specificity, there are differences in their mRNA regulation...

3/3,K/4 (Item 4 from file: 5)  
DIALOG(R)File 5:Biosis Previews(R)  
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09410228 BIOSIS NO.: 199497418598

**Chromosomal localization of four human VH1-like protein-tyrosine phosphatases.**

AUTHOR: Martell Karen J; Kwak Seung; Hakes David J; Dixon Jack E(a); Trent Jeffrey M

AUTHOR ADDRESS: (a)Dep. Biol. Chemistry, University Michigan Med. Center, 5416 Med. Science Building I, Ann Arbor, \*\*USA

JOURNAL: Genomics 22 (2):p462-464 1994

ISSN: 0888-7543

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

QH 426. G46

...ABSTRACT: genes were localized to unique regions of different chromosomes: CL100, a stress-induced PTPase, to 5q35; PAC-1, a mitogen-induced nuclear PTPase, to 2q11; \*hVH\*--\*3\* to 10q25; and hVH-4 to 10q11.

3/3,K/5 (Item 1 from file: 34)  
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci  
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03724792 Genuine Article#: QB156 No. References: 30

**Title: MULTIPLE DUAL-SPECIFICITY PROTEIN-TYROSINE PHOSPHATASES ARE EXPRESSED AND REGULATED DIFFERENTIALLY IN LIVER-CELL LINES**

Author(s): KWAK SP; DIXON JE

Corporate Source: UNIV MICHIGAN, DEPT BIOL CHEM, RM 5416, MED SCI BLDG 1/ANN ARBOR//MI/48109; UNIV MICHIGAN, DEPT BIOL CHEM/ANN ARBOR//MI/48109

Journal: JOURNAL OF BIOLOGICAL CHEMISTRY, 1995, V270, N3 (JAN 20), P 1156-1160

ISSN: 0021-9258

Language: ENGLISH Document Type: ARTICLE (Abstract Available)

...Abstract: other PTPases they exhibit dual catalytic activity toward phosphotyrosine and nearby phosphothreonine residues in substrate proteins. We have isolated a novel VH-1-like PTPase, \*hVH\*--\*3\*, from the human placenta and compared various aspects of its expression with previously isolated members of this subfamily. The mammalian members of this subfamily including \*hVH\*--\*3\* commonly localize to the nucleus and exhibit catalytic activity toward phosphorylated extracellular signal-regulated kinase. However, while the expression of some VH-1-like PTPases is extremely transient and independent of protein synthesis, \*hVH\*--\*3\* expression is sustained over 3 h after being cell stimulated. Tissue-specific expression of \*hVH\*--\*3\* is also distinct from other VH-1-like PTPases. Although VH-1-like PTPases have overlapping substrate specificity, there are differences in their mRNA regulation...

Set	Items	Description
S1	0	(DUSP (W) 5)
S2	23	HVH (W) 3
S3	5	RD (unique items)
S4	294	B23 AND PHOSPHATASE?
S5	48	S4 AND (NUCLEIC (W) ACID?)
S6	48	RD (unique items)
S7	45	S6 AND SEQUENCE?
S8	4	S7 AND THREONINE? AND TYROSINE?

>>>KWIC option is not available in file(s): 41, 77, 399

8/3,K/1 (Item 1 from file: 370)  
 DIALOG(R) File 370:Science  
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00509950 (USE 9 FOR FULLTEXT)

**Type III Secretion Machines: Bacterial Devices for Protein Delivery into Host Cells**

Galan, Jorge E.<CRF RID="C1"> ; Collmer, Alan  
 Section of Microbial Pathogenesis, Boyer Center for Molecular Medicine,  
 Yale School of Medicine, New Haven, CT 06536, USA. Department of Plant  
 Pathology, Cornell University, Ithaca, NY 14853-4203, USA.  
 Science Vol. 284 5418 pp. 1322  
 Publication Date: 5-21-1999 (990521) Publication Year: 1999  
 Document Type: Journal ISSN: 0036-8075  
 Language: English  
 Section Heading: REVIEWS  
 Word Count: 5376

(THIS IS THE FULLTEXT)

...Text: outer membrane. Consequently, these bacteria have evolved a variety of mechanisms to transfer proteins from the cytoplasm to the extracellular environment (B2) . The discovery of \*sequence\* homologies between proteins implicated in the secretion of virulence factors in several different bacterial pathogens and proteins implicated in the export of flagellar components prompted...

...often have a GC content that deviates from that of the chromosome of the host organism, and they are usually bounded by remnants of insertion \*sequences\*, bacteriophage genes, or transposable elements. Amino acid \*sequence\* comparison of the most conserved components of type III secretion and flagellar export systems shows a clustering of different family members in discrete groups (Fig...highly conserved (B1) . These components can be divided into at least two groups. One group consists of predicted outer membrane proteins, including a protein with \*sequence\* similarity to the secretin family of protein transporters, as well as several less conserved lipoproteins. The other group consists of several integral membrane proteins with...

...and two lipoproteins, PrgH and PrgK. Despite the architectural similarity between flagella and type III systems, the structural components of the needle complex share limited \*sequence\* similarity with components of the flagellar basal body (B8) . Although information on the supramolecular organization of type III secretion systems from other bacteria is currently not available, the high degree of \*sequence\* similarity among several structural components indicates that all these systems are likely to have a similar architecture...

...triphosphate (ATP) hydrolysis provides the energy for the secretion process. This is supported by the observation that a conserved component of the secretion systems shares \*sequence\* similarity with the  $\alpha$  and  $\beta$  subunits of the F1 component of the bacterial FOF1 proton-translocating ATPase and that in at least two systems...signal must reside in the structure of the mRNA because mutations that shifted the reading frame of the putative secretion signal, yielding completely different polypeptide \*sequences\*, were still able to direct secretion through the type III machinery (B14) . The 5 (prime) mRNA regions of some of the yop messages

are predicted...

...secretion-associated chaperones have a rather narrow binding specificity and appear to lack nucleotide-binding or nucleotide-hydrolyzing activities. Although they exhibit little amino acid *\*sequence\** similarity, type III secretion chaperones share a number of properties such as relatively small size (15 to 18 kD), a low isoelectric point, and a *\*B23\**).

...

...macrophage function (B13) . YopH appears to exert its effect by dephosphorylating p130.sup(cas) and focal adhesion kinase, two components of focal adhesions that become *\*tyrosine\** phosphorylated upon (beta) 1-integrin stimulation (B27) . *Pseudomonas aeruginosa* delivers an adenosine diphosphate-ribosylating toxin, ExoS, that targets actin-organizing small guanosine triphosphate (GTP)-binding...

...membrane ruffling, and macropinocytosis, ultimately resulting in bacterial uptake (B29) . The effector proteins include an exchange factor for Rho GTPases (SopE) (B30) , an inositol phosphate *\*phosphatase\** (SopB) (B31) , and an actin-binding protein (SipA) (B32) . SopE acts as an exchange factor for a subset of Rho GTPases, including CDC42 and Rac (B30) . SopB modulates the actin cytoskeleton through its inositol phosphate *\*phosphatase\** activity, which generates a broad range of inositol phospholipids and inositol phosphates with demonstrated signaling capacity (B31) . By binding to actin, SipA decreases its critical...induction of apoptosis is dependent on the function of the type III secreted protein YopJ (YopP), which functions by an unknown mechanism (B37) . YopJ shares *\*sequence\** similarity with effector proteins delivered by type III systems in other bacteria, such as the animal pathogen *S. typhimurium* (AvrA) as well as the phytopathogen...

...significance because the AvrRxv protein has been implicated in the stimulation of the hypersensitive response in plants, which involves the induction of apoptosis. Whether the *\*sequence\** similarity among these effector proteins points at some basic signaling pathway conserved in both animals and plants is an open question that may be answered...inside plant cells, indirectly supporting the hypothesis that type III secretion systems direct their delivery to that site (B43) . For example, (i) the amino acid *\*sequence\** of R gene products that are expected to interact with Avr proteins predict an intracellular localization, (ii) several Avr proteins elicit an R gene-dependent...was constructed from a distance matrix (by the unweighted pair group method using arithmetic averages) as implemented in the GCG software package (B45) . Names of *\*sequences\** correspond to the entries in GenBank...

...ADP-ribosyltransferase

	ExoT	ADP-ribosyltransferase
	ExoY	Adenylate cyclase
<i>S. typhimurium</i>	SopE	Exchange factor for Rho GTPases (such as CDC42 and Rac)
	SopB (SigA)	Inositol phosphate <i>*phosphatase*</i>
	SipA	Binds actin, lowering its critical concentration and stabilizing F-actin
	SptP	<i>*Tyrosine*</i> <i>*phosphatase*</i>
<i>Shigella</i> spp.	IpaB	Activation of caspase-1; binds (beta) 1-integrins and CD44
	IpaA	Binds vinculin
	IpgD	Putative inositol phosphate <i>*phosphatase*</i>
<i>Yersinia</i> spp.	YopE	Unknown
	YopH	<i>*Tyrosine*</i> <i>*phosphatase*</i>
	YpkA	Serine/ <i>*threonine*</i> kinase
	YopJ (YopP)	Unknown
Plant pathogens		
<i>P. syringae</i> pv. tomato	AvrPto	Interacts with Pto (R gene product); activates Pto

Xanthomonas campestris pv. vesicatoria	AvrBs2	serine/*threonine* kinase signaling pathway Interacts with Bs2 R gene product of resistant pepper cultivars; *sequence* predicts ability to synthesize or hydrolyze phosphodiester linkages, which may be involved in its virulence function
X. campestris pv. vesicatoria	AvrBs3 family	Localized to plant nuclei; probable transcription factors; activity determined by multiple repeats of 34 amino-acid *sequence*

End Table: Columns 1 - 3 of 4  
Begin Table : Columns 4 - 4 of 4

-----  
Caption:

Examples of effector proteins of known function secreted...

References and Notes:

...Devereux, J., Haeberli, P., Smithies, O., \*Nucleic\* \*Acids\* Res., 12 1984, 387...

8/3,K/2 (Item 2 from file: 370)

DIALOG(R)File 370:Science

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00508367 (USE 9 FOR FULLTEXT)

**Comparison of the Complete Protein Sets of Worm and Yeast: Orthology and Divergence**

Chervitz, Stephen A.; Aravind, L.; Sherlock, Gavin; Ball, Catherine A.; Koonin, Eugene V.; Dwight, Selina S.; Harris, Midori A.; Dolinski, Kara; Mohr, Scott; Smith, Temple; Weng, Shuai; Cherry, J. Michael; Botstein, David

S. A. Chervitz, G. Sherlock, C. A. Ball, S. S. Dwight, M. A. Harris, K. Dolinski, S. Weng, J. M. Cherry, and D. Botstein are in the Department of Genetics, Stanford University School of Medicine, Stanford, CA 94305-5120, USA. L. Aravind and E. V. Koonin are at the National Center for Biotechnology Information, National Library of Medicine, National Institutes of Health, Bethesda, MD 20894, USA. S. Mohr and T. Smith are in the Department of Biomedical Engineering, Boston University, Boston, MA 02115, USA.

Science Vol. 282 5396 pp. 2022

Publication Date: 12-11-1998 (981211) Publication Year: 1998

Document Type: Journal ISSN: 0036-8075

Language: English

Section Heading: Special Section

Word Count: 4794

(THIS IS THE FULLTEXT)

...Abstract: Comparative analysis of predicted protein \*sequences\* encoded by the genomes of *Caenorhabditis elegans* and *Saccharomyces cerevisiae* suggests that most of the core biological functions are carried out by orthologous proteins (proteins...

Text: The nematode worm *Caenorhabditis elegans* is only the second eukaryote to have its genome completely \*sequenced\* (B1) . The first complete eukaryotic genome \*sequence\*, that of the budding yeast *Saccharomyces cerevisiae*, has been reported previously (B2) . Thus, for the first time, it is possible to compare the entire complements...

...The first result is quite surprising: Simple \*sequence\* comparisons allow one to predict, more often than not, orthologous pairs. In many cases, orthologous pairs can be confidently delineated even within families

of highly...

...as described in Table 1. The ORFs within each group were then ordered by similarity clustering with the CLUSTALW program (B14) and displayed as multiple \*sequence\* alignments, rooted cluster dendrograms, and unrooted trees. Each of these displays for every comparison can be found on our Web site. The numbers of worm and yeast ORFs that fall into these clusters at various similarity thresholds are given in Table 1. Figure 1 graphically depicts the distribution of the \*sequences\* from the worm-yeast clusters within functional categories. The first significant (and somewhat unexpected) observation is that the absolute number of ORFs for which we...  
...is not accounted for by endless close variations in the clusters found among the shared set, but instead are proteins that are substantially different in \*sequence\* [compare with (B15)] and thus are likely to perform tasks that are specific to each organism. A subset of such organism-specific proteins, those associated...

...annotation that exists almost exclusively for yeast) might be transferable to the worm, provided that the orthologs between the two species are easily recognizable by \*sequence\* analysis alone. Functional conservation of proteins from different species was first demonstrated experimentally by showing that the mammalian RAS protein can substitute for yeast RAS...

...Table 1 shows that at each level of significance roughly half (611 of 1171 at  $P < 10^{-10}$ ) of all the \*sequence\* similarity groups found by our reciprocal BLASTP procedure contain exactly two members. Because ascertainment of each group began with a yeast-worm HSP, these groups contain one worm and one yeast member. The availability of complete \*sequences\* for both worm and yeast makes it unlikely that we are missing large numbers of potential orthologs. It remains possible that the conservative similarity cutoffs...

...this instance, most of the cases for pairing are conclusive, because the RNA polymerase I and II subunits were independently identified in yeast and worm (\*B23\*). In addition, the cluster [here done at  $P < 10^{-20}$  (B24)] contains the yeast polymerase III subunit paired with its presumed ortholog in the...of proteasome subunits (B26). In this case there are 25 members of the cluster, which form 10 clear pairs, with three yeast and two worm \*sequences\* apparently unpaired. However, it seems probable that there is an additional orthology: yeast PRE2 with the minimally diverged (recently duplicated?) worm \*sequences\* K05C4.1 and Y105E8A.jj. Accepting this, the 25 \*sequences\* yield 11 pairs...

...case of the worm apparently missing orthologs for a set of important yeast proteins. Comparisons were performed with PSI-BLAST (B33) and validated by demonstrating \*sequence\* similarity to *Escherichia coli* or *Methanococcus jannaschii* protein \*sequences\*. A total of 108 mitochondrial proteins from yeast have highly conserved homologs in worm (P-value scores  $< 10^{-39}$ ). These orthologous pairs can be...emerge from these results is that annotation of protein functions and activities will be reliably transferable between organisms as disparate as yeast and worm by \*sequence\* analysis. With well-annotated genomes, the identification of orthologous pairs becomes a powerful analytical approach. Whereas biochemical and biological experiments must be done to unequivocally prove the functions of proteins, the wealth of data from \*sequence\* analyses allows researchers to better design experiments and avoid duplication of work done in other systems...indicated by the conservation of the entire domain architecture of the SH2-containing transcription factor Spt6p. However, the best known role of SH2, in the \*tyrosine\* phosphorylation signaling system, is clearly an innovation for which this domain had been recruited only in animals...

...domains, such as the intracellular domains (MATH, POZ, PDZ, and LIM), and the largely extracellular domains (FN3, LRR, and vWA); (ii) the phosphotyrosine signaling system-\*tyrosine\* kinases, phosphotyrosine \*phosphatases\*, SH2, and PTB (two types of phosphotyrosine-binding domains; the PTB domain was not detected in yeast); (iii) the cyclic nucleotide monophosphate (cNMP)-dependent signaling...





## Figure F2

Caption: Orthologous core biological functions in yeast and worm.

Representative \*sequence\* groups are shown as rooted CLUSTALW

Neighbor-Joining trees, clustered as described in the legend to Table 1, at a similarity level indicated after each...

...site. The axes show the number of proteins with the given domain per 1000 genes. 1, POZ domains; 2, EGF; 3, MATH domain; 4, phosphotyrosine \*phosphatase\*; 5, homeodomains; 6, leucine-rich repeats; 7, calmodulin; 8, PDZ domains; 9, voltage-gated channels; 10, ankyrin repeats; 11, RING domain; 12, C6 fingers; 13, nuclear hormone receptors; 14, AAA-type ATPases. The two domains that are most abundant in yeast, namely serine-\*threonine\* protein kinases and WD40 domains (Table 2), were not used for this plot, in order to improve resolution for the other points...

## References and Notes:

...multiple domains that have a degree of evolutionary independence and are found in different combinations. Thus, the detection of even very high similarity between protein \*sequences\* from two species does not guarantee that the proteins in question are genuine orthologs with a conserved domain architecture (B10) . To diminish (but not eliminate...

...28 October version of the SGD (both are available from the Science Web site as well as SGD). Because the prediction of *C. elegans* protein \*sequences\* had, on 16 October, yet to be corrected by rigorous experimental analysis, our reliance on these predictions may result in the loss of some subset six frame translations of the entire worm DNA \*sequence\* (finished \*sequence\* from the Sanger Centre Web site as of 3 November 1998) and identified no additional homologs at the  $P < 10^{-10}$  level with the...

...14. Thompson, J. D., Higgins, D. G., Gibson, T. J., \*Nucleic\* \*Acids\* Res., 22 1994, 4673...though the similarity of these to RNA polymerases is, upon further study, clearly spurious. This artifact, due to low complexity in the Spt5p amino acid \*sequence\*, is avoidable by more aggressive filtering, applying the >80% alignment requirement as well as increasing the stringency; each of these measures exacts a cost in33. Altschul, S. F., et.al. \*Nucleic\* \*Acids\* Res., 25 1997, 3389 ...

...38. To obtain robust counts for each of the domains in the yeast and worm protein sets, we compared representative \*sequences\* of each domain to the nonredundant protein database (National Center for Biotechnology Information, National Institutes of Health, Bethesda, MD) using the PSI-BLAST program, and the resulting position-dependent weight matrices (profiles) were saved. The number of search iterations and the cutoff for inclusion of \*sequences\* in the profile were adjusted individually for each domain. For most widespread domains, several profiles were constructed to ensure complete coverage. The profiles were then...the collaborations, and K. Anders for helpful discussions. We are especially grateful to R. Durbin (Sanger Centre) and L. Hillier (Genome Sequencing Center) for providing \*sequence\* information and for their cooperation. The SGD is supported by a P41 national resources grant HG01315, from the National Human Genome Research Institute at the...

8/3,K/3 (Item 3 from file: 370)

DIALOG(R)File 370:Science

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00506906 (USE 9 FOR FULLTEXT)

## Exploiting Chemical Libraries, Structure, and Genomics in the Search for Kinase Inhibitors

Gray, Nathanael S.; Wodicka, Lisa; Thunnissen, Andy-Mark W. H.; Norman, Thea C.; Kwon, Soojin; Espinoza, F. Hernan; Morgan, David O.; Barnes, Georjana; LeClerc, Sophie; Meijer, Laurent; Kim, Sung-Hou; Lockhart, David J.; Schultz, Peter G.

N. S. Gray, T. C. Norman, S. Kwon, P. G. Schultz, Howard Hughes Medical

Institute, University of California, Berkeley, CA 94720, USA. L. Wodicka and D. J. Lockhart, Affymetrix, 3380 Central Expressway, Santa Clara, CA 95051, USA. A.-M. W. H. Thunnissen and S.-H. Kim, Lawrence Berkeley National Laboratory and Department of Chemistry, University of California, Berkeley, CA 94720, USA. F. Hernan Espinoza and D. O. Morgan, Department of Physiology, University of California, San Francisco, CA 94143-0444, USA. G. Barnes, Department of Molecular and Cellular Biology, University of California, Berkeley, CA 94720, USA. S. LeClerc and L. Meijer, CNRS, Station Biologique, 29682 Roscoff, France.

Science Vol. 281 5376 pp. 533

Publication Date: 7-24-1998 (980724) Publication Year: 1998

Document Type: Journal ISSN: 0036-8075

Language: English

Section Heading: Reports

Word Count: 4195

(THIS IS THE FULLTEXT)

...Text: to generate small molecule libraries using combinatorial chemistry methods coupled with high-throughput screening, (ii) the enormous increase in the number of newly identified gene \*sequences\* from a host of different organisms, and (iii) the use of structural methods for the detailed characterization of ligand-protein interaction sites that can be ...the acidic C8 atom of the purine ring and the carbonyl oxygen of Glu.sup(81), an infrequently observed interaction in the crystal structures of \*nucleic\* \*acids\* and proteins (B13...a positive feedback loop driving CLB1/2 transcription (B22) . Similarly, CDK activity has been implicated in transcriptional regulation of histone genes including HTA2 and HTB2 (\*B23\*) , and EGT2, a gene involved in the timing of cell separation after cytokinesis...

...on the Pho85p kinase complex to modulate the activity of a transcription factor or factors that regulate a variety of genes, including a secreted acid \*phosphatase\* (Pho5p) (B24) , genes involved in the stress response (the heat shock protein HSP12 and ubiquitin UBI4), and genes involved in glycogen metabolism. Proteins whose transcript...3,800

cGMP-dependent protein kinase	>10,000	>100,000
Casein kinase 1	>3,333	>3,333
GSK3- (beta)	>10,000	>10,000
Insulin-receptor *tyrosine* kinase	5,000	2,200
cCasein kinase 2	>10,000	>10,000
Raf kinase	>1,000	>10,000
v-abl	>10,000	>100,000
cdc28...		

...YDR406w (PDR15); YDL223c (unknown); YER150w (similar to Sed1p an abundant cell surface glycoprotein); YGR032W (GSC2, component of (beta) -1,3-glucan synthase); YGL179C.sup(\*) (serine-\*threonine\* kinase similar to Elm1p and Kin82p); YLR178C (TFS1, Cdc25-dependent nutrient and ammonia response cell cycle regulator); YNR009W (unknown); YFL031W (HAC1, basic leucine zipper protein...with Pho80p or Pho85p); YFL014W (HSP12, heat shock protein); YHR071W (PCL5, cyclinlike and associates with Pho85p); YGR088W (CTT1, cytosolic catalase T); YBR093c (PHO5, secreted acid \*phosphatase\*); YLL039c (UBI4, ubiquitin); YCL009c (PHO84, phosphate transporter); YML116W (PHO8, vacuolar alkaline \*phosphatase\*); YBR296c (homologous to a phosphate-repressible permease). (C) Transcripts that change for cdc28-4, cdc28-4 and 52, cdc28-4 and flavopiridol, and 52: YBR147W...

8/3,K/4 (Item 4 from file: 370)

DIALOG(R) File 370:Science

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00501521 (USE 9 FOR FULLTEXT)

**Inducible Expression and Phosphorylation of Coactivator BOB.1/OBF.1 in T Cells**

Zwilling, Stefan; Dieckmann, Andreas; Pfisterer, Petra; Angel, Peter; Wirth, Thomas

S. Zwilling, P. Pfisterer, T. Wirth, MSZ, Institut fuer Medizinische Strahlenkunde und Zellforschung, Universitaet Wuerzburg, Versbacher Strasse 5, 97078 Wuerzburg, Germany. ; A. Dieckmann and P. Angel, DKFZ, Deutsches Krebsforschungszentrum, Abteilung Signaltransduktion und Wachstumskontrolle, Im Neuenheimer Feld 280, 69120 Heidelberg, Germany.

Science Vol. 277 5323 pp. 221

Publication Date: 7-11-1997 (970711) Publication Year: 1997

Document Type: Journal ISSN: 0036-8075

Language: English

Section Heading: Reports

Word Count: 2610

(THIS IS THE FULLTEXT)

...Text: and Roeder, and they suggested that the 35-kD form might represent a modified version of the 34-kD polypeptide (B6) . Treatment of extracts with \*phosphatases\* did not convert the 35 kD band to the 34 kD band, however (B19...OBF.1 in B cells and T cells, respectively, are virtually identical (Fig. 4 , A and C). All of these phosphorylations occurred on serine and \*threonine\* residues, and no evidence for \*tyrosine\* phosphorylation was obtained (B22) . To determine whether the increased activity correlated with phosphorylation of the COOH-terminal domain, we performed an in vitro phosphorylation assay with the use of purified recombinant BOB.1/OBF.1 COOH-terminal fragment and extracts from unstimulated and stimulated Jurkat T cells (\*B23\*) . In extracts from unstimulated cells, low basal phosphorylation of the fragment encompassing the COOH-terminal 130 amino acids of BOB.1/OBF.1 was observed...

...Fig. 4). Exposure of cells to CsA or FK506 inhibited the effect of PMA and ionomycin. CsA and FK506 are inhibitors of the Ser/Thr-\*phosphatase\* calcineurin; therefore, calcineurin may be a component of the signal transduction pathway leading to the inducible phosphorylation of BOB.1/OBF.1. However, other potential...

...analysis of in vitro phosphorylated GST-BOB.C protein revealed that phosphorylation only occurred at serine residues, suggesting that the phosphorylation that was observed at \*threonines\* in full-length BOB.1/OBF.1 protein occurred within the NH.inf(2)-terminal part of the protein. The domain from amino acids 166...in induced (+) or uninduced (-) Jurkat cell extracts. The scheme (top) shows the COOH-terminal domain of the BOB.1/OBF.1 protein and highlights the \*sequence\* from amino acid 166 to 192, as well as the specific point mutations. (D) GAL4 fusion proteins containing the COOH-terminal 150 amino acids of...

#### References and Notes:

...19. BOB.1/OBF.1 was immunoprecipitated from B cell extracts or induced Jurkat T cell extracts, and precipitates were treated with calf intestinal alkaline \*phosphatase\* or ( $\lambda$ ) \*phosphatase\*. Efficient dephosphorylation was confirmed by including an in vitro phosphorylated protein in some of the samples. Subsequent analysis of the dephosphorylated immunoprecipitates did not show...

...mutated fragments of BOB.1/OBF.1 used for GAL fusion and GST fusion experiments were generated by polymerase chain reaction (PCR) amplification followed by \*sequence\* analysis. Details on the primers used are available upon request. The different subfragments were cloned in frame into either the expression vectors containing the DNA...26. Annweiler, A., Zwilling, S., Wirth, T., \*Nucleic\* \*Acids\* Res., 22 1994, 4250...